Amendments to the Claims

Please amend claims 1, 24 and 28 as indicated in the listing of claims.

The listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently Amended) A method comprising:

a) aligning an object in a parallel manner on a surface by molecular combing;

b) imaging the object by at least two different modalities of scanning probe microscopy (SPM) to obtain data for one or more properties of the object;

c) analyzing the data using a model-based analysis using one or more models of physical structures of known objects;

d) estimating the values of one or more parameters from the data analysis; and

e) fusing the estimated parameters to form a parameter-based characterization of the object.

2. (Previously presented) The method of claim 1, wherein parameter fusion is based on a model of the physical structure of the object.

3. (Canceled)

4. (Previously presented) The method of claim 1, further comprising identifying the object.

5. (Previously presented) The method of claim 4, further comprising comparing the fused parameters with parameters determined from known objects to identify an occurrence of a known object.

6. (Original) The method of claim 1, wherein the SPM imaging includes at least two modalities selected from the group consisting of atomic force microscopy (AFM), scanning tunneling microscopy (STM), lateral force microscopy (LFM), chemical force microscopy (CFM), force modulation imaging, magnetic force microscopy (MFM), high frequency MFM, magnetoresistive sensitivity mapping (MSM), electric force microscopy (EFM), scanning capacitance microscopy (SCM), scanning spreading resistance microscopy (SSRM), tunneling AFM and conductive AFM.

7. (Previously presented) The method of claim 1 wherein the object is a biomolecule.

8. (Original) The method of claim 1, wherein the parameters are estimated by level set techniques, PDE (partial differential equation) techniques and/or active surface techniques.

9. (Original) The method of claim 8, further comprising embedding the techniques in a probabilistic (Bayesian) estimation framework to account for model uncertainty and instrument noise.

10. (Previously presented) The method of claim 1, further comprising classifying the object by applying vector quantization, support vector machines and/or a statistical classifier to the fused parameters.

11. (Original) The method of claim 10, further comprising using known biomolecule structures to generate training sets of data.

12. (Original) The method of claim 7, further comprising using known biomolecule structures to obtain ranges of parameters for each type of biomolecule.

13. (Previously presented) The method of claim 12, wherein the parameter ranges for known biomolecules are used in estimating the parameters.

Claim 14-23. (Canceled)

24. (Currently Amended) A molecular structure identification system comprising:

a) a surface for attachment and alignment of the molecular structures in a parallel manner by molecular combing prior to analysis;

b) a scanning probe microscope with a plurality of imaging modalities configured to obtain data for one or more properties of the molecular structures by at least two different modalities;

c) a controller to control the operation of the scanning probe microscope; and

d) a memory to include one or more characterizations of known molecular structures

25. (Original) The system of claim 24, wherein the characterizations of known structures represent sets of fused parameters derived from a plurality of known biomolecule structures.

26. (Original) The system of claim 25, wherein the characterizations of known structures are used to analyze a set of SPM images.

27. (Canceled)

28. (Currently Amended) The system of claim ~~27~~ 26, wherein the SPM images are analyzed to identify an occurrence of one or more known structures in a sample.

29. (Original) The system of claim 28, wherein the SPM images are analyzed by (i) analyzing a coarse data set to detect locations of potential occurrences of known structures; and (ii) reanalyzing the locations of the potential occurrences one or more additional times, with each analysis utilizing a set of data that is more refined than the set of data utilized in the previous analysis.